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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein . protein database search, using Smith-Waterman algorithm MPsrch_pp

Thu Aug 6 14:06:36 1998; MasPar time 11.35 Seconds 781.822 Million cell updates/sec

Tabular output not generated.

>US-08-813-323A-1

(324-566) from US08813323A.pep (3 of 3) 1764 Description: Perfect Score:

1 SQAEKLKELDKEIRPFRQNW.......YIKDDTIFIKVIVDTSDLPD 243 Sequence:

PAM 150 Gap 11 Scoring table:

120441 seqs, 36531193 residues Searched:

Post-processing:

Minimum Match O% Listing first 45 summaries

Database:

1:pirl 2:pir2 3:pir3 4:pir4 5:nrl3d

Mean 45.997; Variance 110.625; scale 0.416 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

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0; Gaps

Length 567;

Score 1764; DB 2; Length 567 Pred. No. 3.34e-278; 0; Mismatches 0; Indels

Query Match
Best Local Similarity 100.0%;
Matches 243; Conservative

324 SQAEKLKELDKEIRPFRQNWEEADSMKSSVESLQNRVTELESVDKSAGQAARNTGLLESQ 383

384 LSRHDQTLSVHDIRLADMDLRFQVLETASYNGVLIWKIRDYKRRKQEAVMGKTLSLYSQP 443

444 FYTGYFGYKMCARVYLNGDGMGKGTHLSLFFVIMRGEYDALLPWPFKQKVTLMLMDQGSS 503

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SUMMARIES	Ð	I49272	A55960	A55649	153498	161512	S56163	B55649	A54750	138026	A40195	S24134	HYHUMA	HYHOMB	A60364	A42908	A48040	A25561	A45488	S66520	C34787	C39816	8	B34787
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25 25 26 27 28 29 29 111 30 100 31 110 110	33 34 35 36 36 37 37 107 38 107 42 107 42 107 44 107 45 108	AESULT 149272

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#authors Cheng, G.; Cleary, A.M.; Ye, Z.S.; Hong, D.I.; Lederman, S.;
Baltimore, D.
#journal Science (1995) 267:1494-1498
#title Involvement of CRAFI, a relative of TRAF, in CD40 signaling.
#cross-references WUID:95184010
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The Epstein-Barr virus transforming protein LMP1 engages signaling proteins for the tumor necrosis factor receptor
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J. Biol. Chem. (1994) 269:30069-30072
A novel RING finger protein interacts with the cytoplasmic
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TNRR-associated protein LAP1 - human
CD40-binding protein
#formal_name Homo sapiens #common_name man
23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change
10-Sep-1997
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       A55960 #type complete
CD40 receptor-associated factor 1 - human
#formal_name Homo sapiens #common_name man
15-Mar-1996 #sequence_revision 15-Mar-1996 #text_change
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#length 568 #molecular-weight 64459 #checksum 8765
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#authors Sato, T.; Irie, S.; Reed, J.C.
#journal FEBS Lett. (1995) 358:113-118
#title A novel member of the TRAF family of putative signal transducing proteins binds to the cytosolic domain of CD40.
#cross-references MUID:95129692
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#formal_name Homo sapiens #common_name man
02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
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#length 568 #molecular-weight 64490 #checksum 8660
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                                                           ##residues
##cross-references GB:U15637; NID:9595910; PID:9595911
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                             nucleic acid sequence not shown
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##molecule_type mRNA
1-543 ##label RES
domain of CD40.
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Blochem. J. (1995) 309:825-829
Association of a RING finger protein with the cytoplasmic
domain of the human type-2 tumour necrosis factor receptor.
S56163
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tumor necrosis factor receptor-associated protein - human
INF receptor-associated protein
#formal_name Homo sapiens #common_name man
10-0ct-1995 #sequence_revision 01-Dec-1995 #text_change
                                        480 RRHLGDAFKPDPNSSSFKKPTGEMNIASGCPVFVAQTVLENGTYIKDDTIFIKVIVDTSD 539
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Cell (1994) 78:681-692
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Pred. No. 3.24e-112;
51; Mismatches 35; Indels
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T.; Ware, C.; Kieff, E.
T.; Ware, C.; Kieff, E.
The Epstein-Bar: Virus transforming protein LMP1 engages signaling proteins for the tumor necrosis factor receptor
submitted to the EMBL Data Library, July 1994
Association of a RING finger protein with the cytoplasmic
domain of the human type 2 TNF receptor.
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TNFR-associated protein EBI6 - human
#formal_name Homo sapiens #common_name man
23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change
B5649
A55649
                                                                                                                                          ##molecule_type mRNA
##residues
#eross-references EMBL:012597; NID:9975272; PID:9975273
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Pred. No. 3.84e-109;
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Pred. No. 2.05e-98;
50; Mismatches 41; Indels
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Best Local Similarity 51.3%;
Matches 100; Conservative
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A novel family of putative signal transducers associated with the cytoplasmic domain of the 75 kDa tumor necrosis factor
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#title Identification of four novel human genes amplified and overexpressed in breast carcinoma and located to the q11-q21.3 region of chromosome 17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      215 SQLDREHLLSLEQRVVELQQTLAQKDQVLGKLEHSLRLMEEASFDGTFLWKITNVTKRCH 274
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TNF receptor associated factor 1 - mouse
#formal_name Mus musculus #common_name house mouse
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28-Feb-1997
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                                                                                                                                                                                                                                                                                                                                               preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 41.3%; Score 728; DB 2; Length 409; Best Local Similarity 51.8%; Pred. No. 4.48e-98; Matches 101; Conservative 50; Mismatches 40; Indels
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##residues
##coss.references EMBL:X80200; NID:9951276; PID:9951277
                                                                                                                                                                                                                                                                                                                                                                                ##residues 1-409 ##label RES ##cross-references GB:L35302; NID:g532618; PID:g532619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #type complete
protein - human
                                                                                                                                                                                                                                                                                                         #cross-references MUID:94349371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-Aug-1997
I38026; S60681
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548 IKDDTIFIKVIVDTS 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     394 VKDDTMFLKCIVDTS 408
                                                                                                                                                                                                                                                                                            receptor
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#title
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#authors
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                                                                                                          TITLE
ORGANISM
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SUMMARY
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Flannery, A.V.; Macadam, G.C.; Beynon, R.J.
Blochim. Biophys. Acta (1991) 1079:119-122
Immunological characterisation of different meprin species in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #journal J. Bloi. Chem. (1992) 267:9185-9193
#title The alpha subunit of meprin A. Molecular cloning and sequencing, differential expression in inbred mouse strains, and evidence for divergent evolution of the alpha #cross-references MUID:92250517
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                                                        Gaps 7;
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##residues 34-38;78-82 ##label BEY
FICATION #superfamily meprin A; astacin homology; EGF homology; MAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       part of this sequence, including the amino end of the mature protein, was confirmed by protein sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #authors Dumermuth, E.; Sterchi, E.E.; Jiang, W.; Wolz, R.L.; Bond,
J.S.; Flannery, A.V.; Beynon, R.J.
#journal J. Biol. Chem. (1991) 266:21381-21385
#fitle The astacin family of metalloendopeptidases.
#cross-references MUID:92042028
#accession B41196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Beynon, R.J.; Oliver, S.; Robertson, D.H.L.
Blochem. J. (1996) 315:461-466
Characterization of the soluble, secreted form of urinary
                                                                                                                   294 ELRRELEELSVGSDGVLIWKIGSYGRRLQEAKAKPNLECFSPAFYTHKYGYKLQVSAFLN 353
                                                                                                                                                        354 GNGSGEGTHLSLYIRVLPGAFDNLLEWPFARRVTFSLLDQSDPGLAKPQHVTETFHPDPN 413
                                                                                                                                                                                                                                                                     endopeptidase-2
#formal_name Mus musculus #common_name house mouse
16-0ct-1992 #sequence_revision 16-0ct-1992 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A40195 #type complete
meprin A (EC 3.4.24.18) alpha chain precursor - mouse
                                                        44; Mismatches 47; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                              414 WKNFQKPGTWRGSLDESSLGFGYPKFISHQDIRKRNYVRDDAVFIRAAVE 463
Score 437; DB 2; Length 470; Pred. No. 1.59e-49;
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##residues 77-275 ##label DUM
##cross-references GB:M74897; GB:M74238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ##molecule_type mRNA
##residues 1-760 ##label JIA
##cross-references GB:M74897
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#accession S17525
##molecule_type protein
##residues 108,'R',110,'
Query Match 24.8%;
Best Local Similarity 40.0%;
Matches 68; Conservative
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S65552
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75-261
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                                              #domain signal sequence #status experimental #label SIG\
#domain propeptide #status experimental #label PRO\
#product meprin A alpha chain #status experimental
#label MAT\
                                                                                                                                                                                                                                                                                                                             4; Gaps 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Corbell, D.; Gaudoux, F.; Wainwright, S.; Ingram, J.; Kenny, A.J.; Boileau, G.; Crine, P.
FEBS Lett. (1992) 309:203-208-208
Molecular cloning of the alpha-subunit of rat
endopeptidase-24.18 (endopeptidase-2) and co-localization
with endopeptidase-24.11 in rat kidney by in situ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #superfamily meprin A; astacin homology; EGF homology; MAM
  hydrolase; metalloproteinase; transmembrane protein; zinc
                                                                                                                                                                                                                                                                                                                                                                                       447 VWIIRNISQILENTVKGDKL-V-SPRFYNSE-GYGVGVTLYPNGRITSNSGLLGLTFHLY 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    436 VWIIRNISQVLENTVKGDRL-V-SPRFYNSE-GYGFGVTLYPNGRITSNSGYLGLAFHLY 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S24134 #type complete endopeptidase 2 (EC 3.4.24.-) - rat endopeptidase 24.18 endopeptidase 24.18 #formal_name Rattus norvegicus #common_name Norway rat 02-Dec-1993 #sequence_revision 01-Sep-1995 #text_change
                                                                                                                           #domain astacin homology #label AST\
#domain MAM homology #label MAM\
#binding_site zinc (His, His, His, Tyr) #status
predicted\
                                                                                                                                                                                                             #active_site Glu #status predicted
#length 760 #molecular-weight 85702 #checksum 4733
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#domain MAM homology #label MAM\
#binding_site Zinc (His) #startus predicted\
#active_site Glu #status predicted
#active_site Glu #status predicted
#length 748 #molecular-weight 85138 #checksum 2333
                                                                                                                                                                                                                                                                             / Match 9.3%; Score 164; DB 2; Length 760; Local Similarity 30.0%; Pred. No. 7.39e-08; nes 27; Conservative 25; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     uvery Match
Best Local Similarity 28.9%; Pred. No. 3.80e-06;
Matches 26; Conservative 23; Mismatches 27: ---
                                                                                                                                                                                                                                                                                                                         25; Mismatches 34; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      504 SGDNDAILEWPVENRQAIMTILDQEADTRN 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       493 SGDNDVILEWPVENEQAIMTILDQEPDARN 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  478 RGEYDALLPWPFKQKVTLM-LMDQGSSRRH 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -748 ##label COR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hybridization.
#cross-references MUID:92371675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ##status preliminary ##molecule_type mRNA
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                                                                                                                                               276-445
167,171,177,226
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ORGANISM
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265-434
156,160,166
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78-760
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KEYWORDS
FEATURE
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#type complete

HYHUMA

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FEBS Lett. (1993) 335:367-375
Cloning of the PABA peptide hydrolase alpha subunit
(PPH-elpha) from human small intestine and its expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #gene GDB:MEPIA
##Cross-references GDB:371059; OMIM:600388
#map_position 6p21.2-6p21.1
#DEX may form homodimers, homotetramers, or heterotetramers with
two alpha chains and two beta chains (see HYHUMB)
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#domain propeptide #status predicted #label PRO\
#product meprin A alpha chain #status predicted #label
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ##molecule_type protein
##residues 66-83 ##label DU2
##note human meprin A alpha chain appears to be expressed in
##note intestine but not in kidney
meprin A (EC 3.4.24.18) alpha chain precursor - human intestinal brush border metalloendopeptidase;
N-benzoyl-L-tyrosyl-p-aminobenzolc acid hydrolase; PABA peptida hydrolase (PPH) alpha chain
#formal_name Homo saplens #common_name man 1994 #sequence_revision 16-Feb-1996 #text_change 05-Sep-1997
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J.S.; Flannery, A.V.; Beynon, R.J.
#journal J. Biol. Chem. (1991) 266:21381-21385
#title The astacin family of metalloendopeptidases.
#cross.references MUID:92042028
#accession A41196
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#domain MAM homology #label MAM\
#domain EGF homology #label EGF\
#domain transmembrane #status predicted #label TRM\
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                                                                                                                                                                                                                                                                                                                                       ##cross-references EMBL:M82962; NID:g535474; PID:g535475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##residues 65-263 ##label DU3
##cross-references GB:M82962; GB:M74238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33-746 ##label DUM
                                                                                                                                                                                                                                                                                       ##molecule_type mRNA
##residues 1-746 ##label ELD
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674-685,679-694,
696-709
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                           ALTERNATE_NAMES
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                                                                                                                                                                                                                                        #submission
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#title
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674-709
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22-65
66-746
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                                                                                              ORGANISM
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#gene #gene #coss-references GDB:371066 #map_rosition 18q12.2-18q12.3 #map_position 18q12.2-18q12.3 may form homodimers, homotetramers, or heterotetramers with two alpha chains (see HYHUMA) and two beta chains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eldering, J.A.; Groenberg, J.; Sterchi, E.E. submitted to the EMBL Data Library, September 1994 Cloning and the PABA-peptide hydrolase beta subunit: coexpression is required for plasma membrane localization of the alpha subunit in COS-1 cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PEBS Lett. (1993) 335:367-375
Cloning of the PABA peptide hydrolase alpha subunit
(PPH-alpha) From human small intestine and its expression
in COS-1 cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #superfamily meprin A; astacin homology; EGF homology; MAM
homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #domain signal sequence #status predicted #label SIG\
#domain propeptide #status predicted #label PRO\
#product meprin A beta chain #status predicted #label
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predicted
#length 700 #molecular-weight 79458 #checksum 916
                                                                         435 VWTVRNFSQVLENTSKGDKLQ--SPRFYNSE-GYGFGVTLYPNSRE-SSG-YLRLAFHVC 489
                                                                                                                    418 IWKIRDYKRRKQEAVMGKTLSLYSQPFYTGYFGYKMCARVYLNGDGMGKGTHLSLFFVIM 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dumermuth, E.; Eldering, J.A.; Gruenberg, J.; Jiang, W.; Sterchi, E.E.
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#domain MAW homology #label MAM\
#domain EGF homology #label EGF\
#domain Lansmembrane #status predicted #label TRW\
                                                                                                                                                                                                                                                                                                              #type complete
meprin A (EC 3.4.24.18) beta chain precursor - human
N-benzoyl-L-tyrosyl-p-aminobenzoic acid hydrolase; PABA
peptide hydrolase (PPH) beta chain
#formal_name Homo sapiens #common_name man
16-Feb-1995 #sequence_revision 16-Feb-1996 #text_change
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#binding_site zinc (His, His, His, Tyr) #status
predicted\
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##reross-references EMBL:X81333; NID:9557645; PID:9557646
Pred. No. 4.05e-04;
21; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ##molecule_type protein
##residues 62-70,'S',72-73,'P',75-79 ##label DUM
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                                                                                                                                                                                                                        478 RGEYDALLPWPFKOK-VTLMLMDQGSSRRH 506
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     larity 28.9%;
Conservative
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       Best Local Similarity
Matches 26; Conser
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445,547,592,692
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608-619,613-628,
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608-643
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62-700
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tropomyosin - migratory locust
#formal_name Locusta migratoria #common_name migratory locust
03-Feb-1993 #sequence_revision 03-Feb-1993 #text_change
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meprin A (EC 3.4.24.18) beta chain - rat
endopeptidase-2 beta chain; meprin beta chain; meprin-a beta
                                                                                                                                                                                                                                                                                                                                                                                                    Krieger, J.; Raming, K.; Knipper, M.; Grau, M.; Mertens, S.;
Breer, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #superfamily meprin A; astacin homology; EGF homology; MAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence extracted from NCBI backbone (NCBIP:107784)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41 EEARALQKKIQTIENDLDQTQESLGQVMAKLEEKEKALQNAESEVAALNRRIQLLEEDLE 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            431 IWHIRNFIQFI-GSPNG-TL--YSPPFYSSK-GYAF--QIYLN---LAHVTNAGIYFHLI 480
                                                                                                         418 INKIRDYKRRKQEAVMGKTLSLYSQPFYTGYFGYKMCARVYLNGDGMGKGTHLSLFFFVIM 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cloning, sequencing and expression of locust tropomyosin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #formal_name Rattus norvegicus #common_name Norway rat
17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #superfamily tropomyosin
coiled coil; heptad repeat
#length 283 #molecular-weight 32439 #checksum 4917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Johnson, G.D.; Hersh, L.B.
J. Biol. Chem. (1992) 267:13505-13512
Cloning a rat meprin cDNA reveals the enzyme is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       heterodimer; hydrolase; metalloproteinase; zinc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 283;
Score 132; DB 1; Length 700;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    not compared with conceptual translation
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                  Pred. No. 9.47e-04;
20; Mismatches 29;
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Pred. No. 2.90e-03;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Insect Biochem. (1990) 20:173-184
                                                                                                                                                        481 SGANDDQLQWPCPWQQATMTLLDQNPDIRQ 510
                                                                                                                                                                                             478 RGEYDALLPWPFK-QKVTLMLMDQGSSRRH 506
                                                                                                                                                                                                                                                                          #type complete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1-283 ##label KRI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.3%;
Local Similarity 21.3%;
les 16; Conservative
Query Match
Best Local Similarity 33.3%;
Matches 30; Conservative
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A42908
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386 RHDQTLSVHDIRLAD 400
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153,157,163,212 SUMMARY

Ouery Match 6.9%; Score 121; DB 2; Length 668; Best Local Similarity 31.6%; Pred. No. 1.98e-02; Matches 24; Conservative 19; Mismatches 26; Indels 7; Gaps 5;

Db 495 QQATMILLDQNPDIRQ 510 | | | | | | | | | Qy 491 QKVTLMLMDQGSSRRH 506

Search completed: Thu Aug 6 14:07:10 1998 Job time: 34 secs.

